



SEQUENCE LISTING

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McQueen-Mason, Simon

<120> Modification of Plant Fibres

<130> 2531-1-001

<140> 09/383,579  
<141> 1999-08-25

<150> UK 9818808.9  
<151> 1998-08-29

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<170> PatentIn Ver. 2.1

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caggtttcct tcagaagggt tccgtgtgt aagaaaggag gggtaagggtt caccatcaat 360  
gggcactcct acttcaactt ggtgctgatc accaacgtgg gaggtgctgg tgatgtccat 420  
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tgccctccca acttggccct ctccaacgac aatggcggct ggtgcaacccc ccctctccag 240  
cacttcgata tggccgagcc tgctttcttg cagattgccc agtacaaaagc tgggattgtc 300  
ccggtttcct tcagaagggt tccgtgtgt aagaaaggag gggtaagggtt caccatcaat 360  
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<212> DNA
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tcacaaacta tttcaaata taaacccatt ctt atg gct ttt tct tac tca ccc 174
Met Ala Phe Ser Tyr Ser Pro
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ttc tcc tct ctc ttt ctt cct ttc ttc gtc ttc acc ttc gct 222
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gac tac ggt ggc tgg cag agc ggc cac gcc acc ttt tat ggt ggt ggt 270
Asp Tyr Gly Gly Trp Gln Ser Gly His Ala Thr Phe Tyr Gly Gly Gly
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gac gca tct ggc acc atg ggt gga gct tgt ggg tat ggg aat tta tac 318
Asp Ala Ser Gly Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr
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agc caa ggg tat ggc acg aac acg gtg gcg ctg agc act gcg cta ttt 366
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60 65 70

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aac aat gga tta agt tgt ggt gct tgc ttc gaa atg act tgt aca aac 414
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aac cct cct ctc caa cac ttc gac atg gct gag cct gcc ttc ctt caa Asn Pro Pro Leu Gln His Phe Asp Met Ala Glu Pro Ala Phe Leu Gln 120 125 130 135			558
atc gct caa tac cga gct ggt atc gtc ccc gtc tcc ttt cgt agg gta Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Phe Arg Arg Val 140 145 150			606
cca tgt atg aag aaa ggt gga gtg agg ttt aca atc aat ggc cac tca Pro Cys Met Lys Lys Gly Gly Val Arg Phe Thr Ile Asn Gly His Ser 155 160 165			654
tac ttc aac ctc gtt ttg atc aca aac gtc ggt ggc gca ggc gac gtc Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp Val 170 175 180			702
cac tct gtg tcg ata aag ggg tct cga act gga tgg caa tcc atg tct His Ser Val Ser Ile Lys Gly Ser Arg Thr Gly Trp Gln Ser Met Ser 185 190 195			750
aga aat tgg ggc caa aac tgg caa agc aac aac tat ctc aat ggc caa Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Asn Tyr Leu Asn Gly Gln 200 205 210 215			798
ggc ctt tcc ttt caa gtc act ctt agt gat ggt cgc act ctc act gcc Gly Leu Ser Phe Gln Val Thr Leu Ser Asp Gly Arg Thr Leu Thr Ala 220 225 230			846
tat aat ctc gtt cct tcc aat tgg caa ttt ggc caa acc tat gaa ggc Tyr Asn Leu Val Pro Ser Asn Trp Gln Phe Gly Gln Thr Tyr Glu Gly 235 240 245			894
cct caa ttc taa accatatcag ccacactgct atgactacta ctacttcaca Pro Gln Phe 250			946
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 Ala Thr Phe Tyr Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala  
 35 40 45  
 Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Val  
 50 55 60  
 Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys  
 65 70 75 80  
 Phe Glu Met Thr Cys Thr Asn Asp Pro Lys Trp Cys Leu Pro Gly Thr  
 85 90 95  
 Ile Arg Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Phe Ala Leu Pro

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Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Gln His	Phe Asp Met	
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Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Arg	Ala Gly Ile Val	
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Pro Val Ser Phe Arg Arg Val Pro Cys Met Lys	Lys Gly Gly Val Arg	
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Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val	Leu Ile Thr Asn	
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Val Gly Gly Ala Gly Asp Val His Ser Val Ser Ile	Lys Gly Ser Arg	
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Thr Gly Trp Gln Ser Met Ser Arg Asn Trp Gly Gln	Asn Trp Gln Ser	
195	200	205
Asn Asn Tyr Leu Asn Gly Gln Gly Leu Ser Phe	Gln Val Thr Leu Ser	
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Asp Gly Arg Thr Leu Thr Ala Tyr Asn Leu Val Pro	Ser Asn Trp Gln	
225	230	235
Phe Gly Gln Thr Tyr Glu Gly Pro Gln Phe		240
245	250	